BIOTECHNULOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: _09/806,368A_
Source: _PCT09_
Date Processed by STIC: _4|22|02_

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
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Revised 01/29/2002

RAW SEQUENCE LISTING   ·   DATE: 04/22/2002
PATENT APPLICATION: US/09/806,368A   TIME: 14:21:00

Input Set : A:\447.001.txt
Output Set: N:\CRF3\04222002\I806368A.raw

W--> 6 WO 00/21998 PCT/IB99/01621
W--> 8 1
    13 <110> APPLICANT: Hoechst Marion Roussel
    15 <120> TITLE OF INVENTION: MATURE PROTEIN HAVING ANTAGONIST ACTIVITY AGAINST BONE
    16   MORPHOGENETIC PROTEIN.
    18 <130> FILE REFERENCE: JH98KO11 PCT SEQUENCES IN ENGLISH
C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/806,368A
C--> 21 <141> CURRENT FILING DATE: 2001-03-28
    23 <150> PRIOR APPLICATION NUMBER: 10-288103
    24 <151> PRIOR FILING DATE: 1998-10-09
    26 <160> NUMBER OF SEQ ID NOS: 7
    28 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

    30 <210> SEQ ID NO: 1
    31 <211> LENGTH: 119
    32 <212> TYPE: PRT
    33 <213> ORGANISM: Human
    35 <220> FEATURE:
    36 <221> NAME/KEY: CHAIN
    37 <222> LOCATION: (1)..(119)
    38 <223> OTHER INFORMATION: Mature MP52
    40 <300> PUBLICATION INFORMATION:
    41 <301> AUTHORs: MAKISHIMA, Fusoa
    42   TAKAMATSU, Hiroyuki
    43   MIKI, Hideo
    44   KAWAI, Shinji
    45   KIMURA, Michio
    46   MATSUMOTO, Tomoaki
    47   KATSUURA, Mieko
    48   ENOMOTO, Koichi
    65   O 00/21998 PCT/IB99/01621
    67   2
    69   SATOH, Yusuke
    70 <302> TITLE: Novel protein and process for producing the same.
    71 <310> PATENT DOC NO: WO 96/33215   → 10?
W--> 72 <312> PUBLICATION DATE: 1996-(1-0)24
    73 <313> RELEVANT RESIDUES: 1 TO 119
    75 <400> SEQUENCE: 1
    77   Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala   → misaligned amino acid numbering
E--> 78   1   5   10   15   See error Summary sheet, item 3

RAW SEQUENCE LISTING   DATE: 04/22/2002
PATENT APPLICATION: US/09/806,368A   TIME: 14:21:00

Input Set : A:\447.001.txt
Output Set: N:\CRF3\04222002\I806368A.raw

```
 80       Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
 81                20                  25                  30
 83       Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
 84                35                  40                  45
 86       Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
 87            50                  55                  60
 89       Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
 90        65                  70                  75                  80
 92       Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
 93                    85                  90                  95
 95       Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
 96                   100                 105                 110
 98       Val Glu Ser Cys Gly Cys Arg
 99                115
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 114
103 <212> TYPE: PRT
104 <213> ORGANISM: Human
123 (WO 00/21998 PCT/IB99/01621)        → delete
125 3
128 <220> FEATURE:
129 <221> NAME/KEY: CHAIN
130 <222> LOCATION: (1)..(114)
131 <223> OTHER INFORMATION: Mature BMP-2
133 <300> PUBLICATION INFORMATION:
134 <301> AUTHORS: WANG, Elizabeth A.
135            WOZNEY, John M.
136            ROSEN, Vicki A.
137 <302> TITLE: Novel osteoinductive compositions.
138 <310> PATENT DOC NO: WO 88/00205
139 <312> PUBLICATION DATE: 1988-01-14
140 <313> RELEVANT RESIDUES: 1 TO 114
142 <400> SEQUENCE: 2
144       Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg
145        1                   5                  10                  15
147       His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile
148                20                  25                  30
150       Val Ala Pro Pro Gly Tyr His Ala Phe Tyr CYs His Gly Glu Cys Pro
151                35                  40                  45
153       Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln
154          (50                  55                  60 )
156       Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro (Lys) Ala Cys Cys Val
157        65                  70                  75                  80
159       Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
160                    85                  90                  95
162       Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
163       100                 105                 110
164       Cys Arg
181 (WO 00/21998)                              (PCT/IB99/01621)   → delete
```

W--> 123 (handwritten markings)
W--> 125

E--> 154
E--> 156
E--> 157
E--> 160
E--> 164

(Handwritten annotations:)
→ delete
Invalid amino acid designator
→ amino acid numbering misaligned — same error
→ delete

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,368A

DATE: 04/22/2002
TIME: 14:21:00

Input Set : A:\447.001.txt
Output Set: N:\CRF3\04222002\I806368A.raw

4 — delete

```
E--> 184
     187 <210> SEQ ID NO: 3
     188 <211> LENGTH: 116
     189 <212> TYPE: PRT
     190 <213> ORGANISM: Human
     192 <220> FEATURE:
     193 <221> NAME/KEY: CHAIN
     194 <222> LOCATION: (1)..(116)
     195 <223> OTHER INFORMATION: Mature BMP-4
     197 <300> PUBLICATION INFORMATION:
     198 <301> AUTHORs: WOZNEY, John M.
     199       ROSEN, Vicki
     200       CELESTE, Anthony J.
     201       MITSOCK, Lisa M.
     202       WHITTERS, Matthew J.
     203       KRIZ, Ronald W.
     204       HEWICK, Rodney M.
     205       WANG, Elizabeth A.
     206 <302> TITLE: Novel regulators of bone formation molecular clones
     207       and activities.
     208 <303> JOURNAL: Science
     209 <304> VOLUME: 242
     210 <305> ISSUE: 4885
     211 <306> PAGES: 1528-1534
     212 <307> DATE: 1988-12-16
     213 <308> DATABASE ACCESSION NO: Genbank/M22490
     214 <313> RELEVANT RESIDUES: 1 TO 116
W--> 216 <300> PUBLICATION INFORMATION: 3
     217       Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys
     218        1               5                  10                  15
E--> 220       Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp
E--> 221                   20                  25                  30
     223       Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp
E--> 224                   35                  40                  45
     239       WO 00/21998                                 PCT/IB99/01621
E--> 241                                    5
     244       Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
E--> 245            50                  55                  60
E--> 247       Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser 71 e Pro Lys Ala Cys
E--> 248       65                  70                  75                  80
     250       Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu
E--> 251                        85                  90                  95
     253       Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu met Val Val Glu Gly
E--> 254                      100                 105                 110
     256       Cys Gly Cys Arg
E--> 257                      115
     259 <210> SEQ ID NO: 4
     261 <211> LENGTH: 139
     262 <212> TYPE: PRT
```

[handwritten notes:]
13097 - database entry date is required - per Sect 1.823 of the new Rule.

WO 00/21998 ... PCT/IB99/01621 → delete

71 e → invalid amino acid designator!

```
          RAW SEQUENCE LISTING              DATE: 04/22/2002
          PATENT APPLICATION:  US/09/806,368A    TIME: 14:21:00

               Input Set : A:\447.001.txt
               Output Set: N:\CRF3\04222002\I806368A.raw
```

```
263 <213> ORGANISM: Human
265 <220> FEATURE:
267 <221> NAME/KEY: CHAIN
268 <222> LOCATION: (1)..(139)
269 <223> OTHER INFORMATION: Mature BMP-7
271 <300> PUBLICATION INFORMATION:
273 <301> AUTHORs: OZKAYNAK, Engin
274       RUEGER, David C.
275       DRIER, Eric A.
276       CORBETT, Clare
277       RIDGE, Richard J.
278       SAMPATH, Kuber T.
279       OPPERMANN, Hermann
280 <302> TITLE: OP-1 cDNA encodes an osteogenic protein in the TGF-beta
281       family.
294       WO 00/21998 PCT/IB99/01621
296       6
300 <303> JOURNAL: EMBO J.
301 <304> VOLUME: 9
302 <305> ISSUE: 7
303 <306> PAGES: 2085-2093
304 <307> DATE: 1990
305 <308> DATABASE ACCESSION NO: EM13L data library/X51801
306 <313> RELEVANT RESIDUES: 1 TO 139
```

(handwritten: same error as on p.3)

W--> 308 <300> PUBLICATION INFORMATION: 4   *(handwritten: → requires <3097,)*

```
310       Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
311        1           5                   10                  15
E--> 313  Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala G7-u Asn Ser Ser Ser
314                20                  25                  30
316       Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
317                35                  40                  45
319       Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
320            50                  55                  60
322       Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
E--> 323   65          70                  75                  80
325       Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
E--> 326            85                  90                  95
328       Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
E--> 329            100                 105                 110
331       Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
E--> 332            115                 120                 125
334       Arg Asn Met Val Val Arg Ala Cys Gly Cys His
E--> 335            130                 135
350       WO 00/21998                                    PCT/IB99/01621
E--> 352                              7
355 <210> SEQ ID NO: 5
357 <211> LENGTH: 119
358 <212> TYPE: PRT
359 <213> ORGANISM: Human
```

(handwritten annotations: "G7-u" circled; "misaligned numbering. some error" near line 323; "delete" with arrow near line 350; "PCT/IB99/01621" circled; "WO 00/21998" circled)

RAW SEQUENCE LISTING   DATE: 04/22/2002
PATENT APPLICATION: US/09/806,368A   TIME: 14:21:00

Input Set : A:\447.001.txt
Output Set: N:\CRF3\04222002\I806368A.raw

```
361 <220> FEATURE:
363 <221> NAME/KEY: CHAIN
364 <222> LOCATION: (1)..(119)
365 <223> OTHER INFORMATION: Mature MP52 protein. Note : 30th, 71st, 74th and
366       111th Met are modified to met sulfoxide.                              invalid amino
368 <400> SEQUENCE: 5                                                           acid designate
```

E--> 370   Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
```
371     1                 5                 10                15
373     Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
374                 20                25                30
376     Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
377                 35                40                45
379     Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
380             50                55                60
382     Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
383     65                70                75                80
385     Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
386                 85                90                95
388     Ile Asn Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
389                 100               105               110
391     Val Glu Ser Cys Gly Cys Arg
392                 115
407     WO 00/21998                                      PCT/IB99/01621         — delete
```
E--> 409   8
```
411 <210> SEQ ID NO: 6
412 <211> LENGTH: 119
413 <212> TYPE: PRT
414 <213> ORGANISM: Human
416 <220> FEATURE:
417 <221> NAME/KEY: CHAIN
418 <222> LOCATION: (1)..(119)
419 <223> OTHER INFORMATION: Mature MP52 protein. Note : 30th and/or 71st
420       and/or 74th and/or 111th met are modified to
421       s-carboxymethyl Met.
423 <400> SEQUENCE: 6
425     Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
426     1                 5                 10                15
428     Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
429                 20                25                30
431     Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
432                 35                40                45
434     Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
435             50                55                60
437     Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
438     65                70                75                80
440     Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
441                 85                90                95
443     Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
444                 100               105               110
```

RAW SEQUENCE LISTING   DATE: 04/22/2002
PATENT APPLICATION: US/09/806,368A   TIME: 14:21:00

Input Set : A:\447.001.txt
Output Set: N:\CRF3\04222002\I806368A.raw

```
         446        Val Glu Ser Cys Gly Cys Arg
         447              115
         464        WO 00/21998                          PCT/IB99/01621    —delete
E--> 466                                9
         469  <210> SEQ ID NO: 7
         470  <211> LENGTH: 119
         471  <212> TYPE: PRT
         472  <213> ORGANISM: Human
         474  <220> FEATURE:
         475  <221> NAME/KEY: CHAIN
         476  <222> LOCATION: (1)..(119)
         477  <223> OTHER INFORMATION: Mature MP52 protein. Note :32nd and 35th Trp are
         478        modified to allylsulphenyl Trp.
         480  <400> SEQUENCE: 7
E--> 482        Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
         483         1              5                   10                  15
         485        Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
         486              20                  25                  30
         488        Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
         489              35                  40                  45
         491        Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
         492              50                  55                  60
E--> 494        Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
         495         65                  70                  75                  80
         497        Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
         498              85                  90                  95
E--> 500        Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
         501              100                 105                 110
         503        Val Glu Ser Cys Gly Cys Arg
         504              115
```

circled items are invalid amino acid designators!

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/22/2002
PATENT APPLICATION: **US/09/806,368A**   TIME: 14:21:01

Input Set : **A:\447.001.txt**
Output Set: **N:\CRF3\04222002\I806368A.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 162

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/806,368A

DATE: 04/22/2002
TIME: 14:21:01

Input Set : **A:\447.001.txt**
Output Set: **N:\CRF3\04222002\I806368A.raw**

```
L:6 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:8 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:20 M:270 C: Current Application Number differs, Replaced Application Number
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:72 M:256 W: Invalid Numeric Header Field, Wrong PUBLICATION DATE:YYYY-MM-DD
L:78 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:123 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:125 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:154 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:156 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=2
L:216 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:3
L:220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:247 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:247 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:308 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:4
L:313 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:313 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:323 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:370 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:409 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:466 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:482 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:494 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:500 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
```

PCT09

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 09/806,368A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
  Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
  Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
  "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
  (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
  (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
  (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
  Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
  "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.